

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ni, Jian
Rosen, Craig A.
Gentz, Reiner L.
Lyn, Sally Doreen Patricia
Hurle, Mark Robert
- (ii) TITLE OF INVENTION: Human Tumor Necrosis Factor
Receptor-Like 2
- (iii) NUMBER OF SEQUENCES: 24
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
(B) STREET: 1100 New York Ave, Suite 600
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/464,595
(B) FILING DATE: 05-JUN-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/462,962
(B) FILING DATE: 05-JUN-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/462,315
(B) FILING DATE: 05-JUN-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/US95/05058
(B) FILING DATE: 27-APR-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Steffe, Eric K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.0770004/EKS/SGW
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-271-2600
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1704 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 265..1113

- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 265..372

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 373..1113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCACGAGCTG CCTCCCGCAG GCGCCACCTG TGTCCCCCAG CGCCGCTCCA CCCAGCAGGC	60
CTGAGCCCCT CTCTGCTGCC AGACACCCCC TGCTGCCCCAC TCTCCTGCTG CTCGGGTTCT	120
GAGGCACAGC TTGTCACACC GAGGCGGATT CTCTTTCTCT TTCTCTTTCT CTTCTGGCCC	180
ACAGCCGCAG CAATGGCGCT GAGTTCCTCT GCTGGAGTTC ATCCTGCTAG CTGGGTTCCC	240
GAGCTGCCGG TCTGAGCCTG AGGC ATG GAG CCT CCT GGA GAC TGG GGG CCT	291
Met Glu Pro Pro Gly Asp Trp Gly Pro	
-36 -35 -30	
CCT CCC TGG AGA TCC ACC CCC AAA ACC GAC GTC TTG AGG CTG GTG CTG	339
Pro Pro Trp Arg Ser Thr Pro Lys Thr Asp Val Leu Arg Leu Val Leu	
-25 -20 -15	
TAT CTC ACC TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC	387
Tyr Leu Thr Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser	
-10 -5 1 5	
TGC AAG GAG GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC	435
Cys Lys Glu Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys	
10 15 20	
AGT CCA GGT TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA	483
Ser Pro Gly Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr	
25 30 35	
GTG TGT GAA CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC	531
Val Cys Glu Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly	
40 45 50	

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CTA AGC AAG TGT CTG CAG TGC CAA ATG TGT GAC CCA GCC ATG GGC CTG Leu Ser Lys Cys Leu Gln Cys Gln Met Cys Asp Pro Ala Met Gly Leu 55 60 65	579
CGC GCG AGC CGG AAC TGC TCC AGG ACA GAG AAC GCC GTG TGT GGT TGC Arg Ala Ser Arg Asn Cys Ser Arg Thr Glu Asn Ala Val Cys Gly Cys 70 75 80 85	627
AGC CCA GGC CAC TTC TGC ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG Ser Pro Gly His Phe Cys Ile Val Gln Asp Gly Asp His Cys Ala Ala 90 95 100	675
TGC CGC GCT TAC GCC ACC TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA Cys Arg Ala Tyr Ala Thr Ser Ser Pro Gly Gln Arg Val Gln Lys Gly 105 110 115	723
GGC ACC GAG AGT CAG GAC ACC CTG TGT CAG AAC TGC CCC CCG GGG ACC Gly Thr Glu Ser Gln Asp Thr Leu Cys Gln Asn Cys Pro Pro Gly Thr 120 125 130	771
TTC TCT CCC AAT GGG ACC CTG GAG GAA TGT CAG CAC CAG ACC AAG TGC Phe Ser Pro Asn Gly Thr Leu Glu Glu Cys Gln His Gln Thr Lys Cys 135 140 145	819
AGC TGG CTG GTG ACG AAG GCC GGA GCT GGG ACC AGC AGC TCC CAC TGG Ser Trp Leu Val Thr Lys Ala Gly Ala Gly Thr Ser Ser Ser His Trp 150 155 160 165	867
GTA TGG TGG TTT CTC TCA GGG AGC CTC GTC ATC GTC ATT GTT TGC TCC Val Trp Trp Phe Leu Ser Gly Ser Leu Val Ile Val Ile Val Cys Ser 170 175 180	915
ACA GTT GGC CTA ATC ATA TGT GTG AAA AGA AGA AAG CCA AGG GGT GAT Thr Val Gly Leu Ile Ile Cys Val Lys Arg Arg Lys Pro Arg Gly Asp 185 190 195	963
GTA GTC AAG GTG ATC GTC TCC GTC CAG CGG AAA AGA CAG GAG GCA GAA Val Val Lys Val Ile Val Ser Val Gln Arg Lys Arg Gln Glu Ala Glu 200 205 210	1011
GGT GAG GCC ACA GTC ATT GAG GCC CTG CAG GCC CCT CCG GAC GTC ACC Gly Glu Ala Thr Val Ile Glu Ala Leu Gln Ala Pro Pro Asp Val Thr 215 220 225	1059
ACG GTG GCC GTG GAG GAG ACA ATA CCC TCA TTC ACG GGG AGG AGC CCA Thr Val Ala Val Glu Glu Thr Ile Pro Ser Phe Thr Gly Arg Ser Pro 230 235 240 245	1107
AAC CAC TGACCCACAG ACTCTGCACC CCGACGCCAG AGATACCTGG AGCGACGGCT Asn His	1163
GAATGAAAGA GGCTGTCCAC CTGGCGGAAC CACCGGAGCC CGGAGGCTTG GGGGCTCCAC	1223
CCTGGACTGG CTTCGTCTC CTCCAGTGA GGGAGAGGTG GCGCCCCTGC TGGGGTAGAG	1283
CTGGGGACGC CACGTGCCAT TCCCATGGGC CAGTGAGGGC CTGGGGCCTC TGTTCTGCTG	1343
TGGCCTGAGC TCCCCAGAGT CCTGAGGAGG AGCGCCAGTT GCCCCTCGCT CACAGACCAC	1403

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ACACCCAGCC CTCCTGGGCC AACCCAGAGG GCCTTCAGAC CCCAGCTGTG TGC GCGTCTG 1463
 ACTCTTGTGG CCTCAGCAGG ACAGGCCCCG GGCCTGCCT CACAGCCAAG GCTGGACTGG 1523
 GTTGGCTGCA GTGTGGTGT TAGTGGATAC CACATCGGAA GTGATTTTCT AAATTGGATT 1583
 TGAATTCGGC TCCTGTTTTT TATTTGTCAT GAAACAGTGT ATTTGGGGAG ATGCTGTGGG 1643
 AGGATGTAAA TATCTTGT TT CTCCTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1703
 A 1704

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
 -36 -35 -30 -25
 Lys Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
 -20 -15 -10 -5
 Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
 1 5 10
 Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
 15 20 25
 Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
 30 35 40
 Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
 45 50 55 60
 Gln Met Cys Asp Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser
 65 70 75
 Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile
 80 85 90
 Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser
 95 100 105
 Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr
 110 115 120
 Leu Cys Gln Asn Cys Pro Pro Gly Thr Phe Ser Pro Asn Gly Thr Leu
 125 130 135 140
 Glu Glu Cys Gln His Gln Thr Lys Cys Ser Trp Leu Val Thr Lys Ala
 145 150 155

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 Cont

Gly Ala Gly Thr Ser Ser Ser His Trp Val Trp Trp Phe Leu Ser Gly
 160 165 170
 Ser Leu Val Ile Val Ile Val Cys Ser Thr Val Gly Leu Ile Ile Cys
 175 180 185
 Val Lys-Arg Arg Lys Pro Arg Gly Asp Val Val Lys Val Ile Val Ser
 190 195 200
 Val Gln Arg Lys Arg Gln Glu Ala Glu Gly Glu Ala Thr Val Ile Glu
 205 210 215 220
 Ala Leu Gln Ala Pro Pro Asp Val Thr Thr Val Ala Val Glu Glu Thr
 225 230 235
 Ile Pro Ser Phe Thr Gly Arg Ser Pro Asn His
 240 245

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr
 1 5 10 15
 Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu
 20 25 30
 His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr
 35 40 45
 Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser
 50 55 60
 Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His
 65 70 75 80
 Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr
 85 90 95
 Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr
 100 105 110
 Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly
 115 120 125
 Phe Gly Val Met Glu Met Ala Thr Glu Thr Thr Asp Thr Val Cys His
 130 135 140

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Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys
145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln
165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met
180 185 190

Arg Ala Leu Leu Val Ile Pro Val Val Met Gly Ile Leu Ile Thr Ile
195 200 205

Phe Gly Val Phe Leu Tyr Ile Lys Lys Val Val Lys Lys Pro Lys Asp
210 215 220

Asn Glu Met Leu Pro Pro Ala Ala Arg Arg Gln Asp Pro Gln Glu Met
225 230 235 240

Glu Asp Tyr Pro Gly His Asn Thr Ala Ala Pro Val Gln Glu Thr Leu
245 250 255

His Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile
260 265 270

Ser Val Gln Glu Arg Gln Val Thr Asp
275 280

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 373..927

- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 373..480

- (ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 481..927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCCCTTCTA CAGGAAACCC GGAGTGGAC T GGAACGGTGC AGGGGGAGAA CTCGCCCCCTC 60

CCATCGGGCG CCTCCTTCAT ACCGGCCCTT CCCCTCGGCT TTGCCTGGAC AGCTCCTGCC 120

TCAGGCAGCG CCACCTGTGT CGCCCAGCGC CGCTCCACCC AGCAGGCCTG AGCCCCCTCTC 180

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TGCTGCCAGA CACCCCCTGC TGCCCACTAC TCCTGCTGCT CGGGTTCTGA GGCACAGCTT	240
GTCACACCGA GGC GGATTCT CTTTCTCTTT CTCTTTCTCT TCTGGCCAC AGCCGCAGCA	300
ATGGCGCTGA GTTCCTCTGC TGGAGTTCAT CCTGCTAGCT GGGTTCCCGA GCTGCCGGTC	360
TGAGCCTGAG TC ATG GAG CCT CCT GGA GAC TGG GGG CCT CCT CCC TGG Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp -36 -35 -30 -25	408
AGA TCC ACC CCC AGA ACC GAC GTC TTG AGG CTG GTG CTG TAT CTC ACC Arg Ser Thr Pro Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr -20 -15 -10	456
TTC CTG GGA GCC CCC TGC TAC GCC CCA GCT CTG CCG TCC TGC AAG GAG Phe Leu Gly Ala Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu -5 1 5	504
GAC GAG TAC CCA GTG GGC TCC GAG TGC TGC CCC AAG TGC AGT CCA GGT Asp Glu Tyr Pro Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly 10 15 20	552
TAT CGT GTG AAG GAG GCC TGC GGG GAG CTG ACG GGC ACA GTG TGT GAA Tyr Arg Val Lys Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu 25 30 35 40	600
CCC TGC CCT CCA GGC ACC TAC ATT GCC CAC CTC AAT GGC CTA AGC AAG Pro Cys Pro Pro Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys 45 50 55	648
TGT CTG CAG TGC CAA ATG TGT GAC CCA GAT ATT GGT TCC CCC TGT GAC Cys Leu Gln Cys Gln Met Cys Asp Pro Asp Ile Gly Ser Pro Cys Asp 60 65 70	696
CTC AGG GGA AGA GGT CAC CTG GAG GCT GGT GCC CAC CTG AGT CCA GGC Leu Arg Gly Arg Gly His Leu Glu Ala Gly Ala His Leu Ser Pro Gly 75 80 85	744
AGA CAG AAA GGG GAA CCA GAC CCA GAG GTG GCC TTT GAG TCA CTG AGC Arg Gln Lys Gly Glu Pro Asp Pro Glu Val Ala Phe Glu Ser Leu Ser 90 95 100	792
GCA GAG CCT GTC CAT GCG GCC AAC GGC TCT GTC CCC TTG GAG CCT CAT Ala Glu Pro Val His Ala Ala Asn Gly Ser Val Pro Leu Glu Pro His 105 110 115 120	840
GCC AGG CTC AGC ATG GCC AGT GCT CCC TGC GGC CAG GCA GGA CTG CAC Ala Arg Leu Ser Met Ala Ser Ala Pro Cys Gly Gln Ala Gly Leu His 125 130 135	888
CTG CGG GAC AGG GCT GAC GGC ACA CCT GGG GGC AGG GCC TGAGCCTACA Leu Arg Asp Arg Ala Asp Gly Thr Pro Gly Gly Arg Ala 140 145	937
GGGAGGCACA GGGCAGGTGG GCTAGCCATG AACAGAAGAG GAAGCTGGAG TGCTTTGGGG	997
GTTTCATGCAT GTAGGCTGGG ATTTGGGGCT CACACCTCAA CCTGCATGCC CAGTTCCATG	1057
CCCCTCCCCT CTTGTGAAAG CACCTGTCTA CTTGGGCTGA GGATGTGGGG GCACAGGTGG	1117

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Cont.

CAGGTGAGGC	TGCCCTCAGG	AGGGGCCCCAG	GCCCAGCTTG	TACCCACCT	CCACCAGTAC	1177
CTGAAGAAGT	GGGGCTCTCA	CCCTACCTGC	CTCTGCCATT	GGAATGGCCT	GGTTTGCACA	1237
GATGGGAAAC	CCGTTTGAGG	GGTGGGTGTC	TGGGTGGGCA	CGTGGGGCGA	GGACCTGCCT	1297
GAGGGACCCT	GCCCTGGAAC	TGACAGTGCA	AGCTEGGCGT	CCTGCCCATC	TGGGCAGAAG	1357
GCTGGTTTCT	CCCATCAACG	AAGCCCTCCC	AGGACCTTCC	TGCAAGCCCT	CGTCCCACAC	1417
GCAGCTCTGC	CGTCCCTTGG	TGTCCCTCCC	GGCCTCAGGT	CCTCCATGCT	GGGTACCTCT	1477
GGGCACCTCG	TTTGGCTGAG	CCAGGGGTTC	AGCCTGGCAG	GGCGCCCTGG	CAGCAGTCCT	1537
TGGCCTGTGG	ATGCTGTCCT	GGCCTGTGGA	TGGTGTCCCG	CCCTCCACGT	ACCCCTCTCA	1597
CCCCCTCCTC	TTGGACTCCA	GCCATGGGCC	TGCGCGCGAG	CCGGAAGTGC	TCCAGGACAG	1657
AGAACGCCGT	GTGTGGCTGC	AGCCCAGGCC	ACTTCTGCAT	CGTCCAGGAC	GGGGACCACT	1717
GCGCCGCGTG	CCGCGCTTAC	GCCACCTCCA	GCCCAGGCCA	GAGGGTGCAG	AAGGGAGGCA	1777
CCGAGAGTCA	GGACACCCTG	TGTCAGAACT	GCCCCCGGG	GACCTTCTCT	CCCAATGGGA	1837
CCCTGGAGGA	ATGTCAGCAC	CAGACCAATT	GGCCTAATCA	TATGTGTGAA	AAGAAGAAAG	1897
CCAAGGGGTG	AGCACACGGT	GGCCCCATCA	GGGTTCATGT	CCCCAGCCGT	CACCTCTTGG	1957
AGCTCTGTCA	CCCCAAGCCT	GGGAGGTGGC	CCCAGAGCTT	TTCCAGGATC	CGCGGCTCCT	2017
CCCAGGGCAG	CCACTGCAGG	CTGGGGCAGG	TGTATGTAGT	CAAGGTGATC	GTCTCCGTCC	2077
AGCGGTAAAA	GACAGGAGGC	AGAAGGTGAG	GCCACAGTCA	TTGAGCCCTG	CAGGCCCCCTC	2137
CGGACGTCAC	CACGGTGGCC	GTGGAGGAGA	CAATACCCTC	ATTCACGGGG	AGGAGCCCAA	2197
ACCACTGACC	CACAGACTCT	GCACCCCGAC	GCCAGAGATA	CCTGGAGAGA	CGGCTGCTGA	2257
TAGAGGCTGT	CCACCTGGCG	AAACCACCGG	AGCCCGGAGG	CTTGGGGGCT	CCGCCCTGGG	2317
CTGGTTTCCG	TCTCCTCCAG	TGGAGGGAGA	GGTGGTGCCC	CTGCTGGTGG	TAGAGCTGGG	2377
GACGCCACGT	GCCATTCCCA	TGGTTCAGTG	AGGGGCTGGT	GGCCTCTGTT	CTGCTGTGGC	2437
CTGAGCTCCC	CAGAGTCCTG	AGGAGGAGCC	CCAGTTGCCC	CTCGCTCACA	GACCACACAC	2497
CCAGCCCTCC	TGGGCCAACC	CAGAGGCCCC	TTCAGACCCC	AGCTGTCTGC	GCGTCTGACT	2557
CTTGTGGCCT	CAGCAGGACA	GGCCCCGGGC	ACTGCCTCAC	AGCCAAGGCT	GGAATGGGTT	2617
GGCTGCAGTG	TGGTGTTTAG	TGGATACCAC	ATCGGAAGTG	ATTTTCTAAA	AATTGGATTT	2677
GAATTCGGAA	AAAAA					2692

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Pro Pro Gly Asp Trp Gly Pro Pro Pro Trp Arg Ser Thr Pro
-36 -35 -30 -25
Arg Thr Asp Val Leu Arg Leu Val Leu Tyr Leu Thr Phe Leu Gly Ala
-20 -15 -10 -5
Pro Cys Tyr Ala Pro Ala Leu Pro Ser Cys Lys Glu Asp Glu Tyr Pro
1 5 10
Val Gly Ser Glu Cys Cys Pro Lys Cys Ser Pro Gly Tyr Arg Val Lys
15 20 25
Glu Ala Cys Gly Glu Leu Thr Gly Thr Val Cys Glu Pro Cys Pro Pro
30 35 40
Gly Thr Tyr Ile Ala His Leu Asn Gly Leu Ser Lys Cys Leu Gln Cys
45 50 55 60
Gln Met Cys Asp Pro Asp Ile Gly Ser Pro Cys Asp Leu Arg Gly Arg
65 70 75
Gly His Leu Glu Ala Gly Ala His Leu Ser Pro Gly Arg Gln Lys Gly
80 85 90
Glu Pro Asp Pro Glu Val Ala Phe Glu Ser Leu Ser Ala Glu Pro Val
95 100 105
His Ala Ala Asn Gly Ser Val Pro Leu Glu Pro His Ala Arg Leu Ser
110 115 120
Met Ala Ser Ala Pro Cys Gly Gln Ala Gly Leu His Leu Arg Asp Arg
125 130 135 140
Ala Asp Gly Thr Pro Gly Gly Arg Ala
145

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu

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1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser
245

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2637 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

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(A) NAME/KEY: CDS
(B) LOCATION: 247..654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAGCTCGGG CTCCACCGGG GACGACCGCT CCTAGAAACT GAGTGGTATC CCCCGGGCGCT	60
GCAGGAATTC CAACCTGCCT GAAGGGACCC TGCCCTGGAA CTGACAGTGC AAGCTCGGCG	120
TCCTGCCCAT CTGGGAAGAA GGCTGGTTTC TCCCATCAAC GAAGCCCTCC CAGGACCTTC	180
CTGCAAGCCC TCGTCCCACA CGCAGCTCTG CCGTCCCTTG GTGTCCCTCC CGGCCTCAGG	240
TCCTCC ATG CTG GGT ACC TCT GGG CAC CTC GTT TGG CTG AGC CAG GGG	288
Met Leu Gly Thr Ser Gly His Leu Val Trp Leu Ser Gln Gly	
150 155 160	
TTC AGC CTG GCA GGG CGC CCT GGC AGC AGT CCT TGG CCT GTG GAT GCT	336
Phe Ser Leu Ala Gly Arg Pro Gly Ser Ser Pro Trp Pro Val Asp Ala	
165 170 175	
GTC CTG GCC TGT GGA TGG TGT CCC GGC CTC CAC GTA CCC CCT CTC AGC	384
Val Leu Ala Cys Gly Trp Cys Pro Gly Leu His Val Pro Pro Leu Ser	
180 185 190 195	
CCC TCC TCT TGG ACT CCA GCC ATG GGC CTG CGC GCG AGC CGG AAC TGC	432
Pro Ser Ser Trp Thr Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys	
200 205 210	
TCC AGG ACA GAG AAC GCC GTG TGT GGC TGC AGC CCA GGC CAC TTC TGC	480
Ser Arg Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys	
215 220 225	
ATC GTC CAG GAC GGG GAC CAC TGC GCC GCG TGC CGC GCT TAC GCC ACC	528
Ile Val Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr	
230 235 240	
TCC AGC CCG GGC CAG AGG GTG CAG AAG GGA GGC ACC GAG AGT CAG GAC	576
Ser Ser Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp	
245 250 255	
ACC CTG TGT CAG AAC TGC CCC CGG GGA CCT TCT CTC CCA ATG GGA CCC	624
Thr Leu Cys Gln Asn Cys Pro Arg Gly Pro Ser Leu Pro Met Gly Pro	
260 265 270 275	
TGG AGG AAT GTC AGC ACC AGA CCA AGT AAG TGAACCCGGG GGAGGCCAGC	674
Trp Arg Asn Val Ser Thr Arg Pro Ser Lys	
280 285	
TCTGTGCCCT GGGGAGGGGG CTCCACGTTG CTTCCCTGGG AGATGACCGT CTTCTCCAGC	734
AGAAAGGTTG AAGGTCCCAC CCTGAGCGGC ACCCTGGTCA CATGCCTGCG TCCAGGAGAG	794
CTGCAGGGTG AAGCCTGTGT GCCCCAGATA ACCCCTTCCA TGGGCCCAGA CAAAGCCTCA	854
TCAGATCTGA GCTTCCTGGA GGCTCAGGAT GGGCCTTCCC AGAAGCAGGC CCAGAGGGAG	914
GCTGCCTCCA GATCCCCTGT CCCCTGGGGC TGTGGGTGTC CCTGAATGTC AGGGCCATGG	974

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cont.

GAGGGCCCCT	GGGCTTCAGG	GGTTGGGGAA	AGTGAACACT	CTGCTCTTTG	TCCACCTTCG	1034
GGAGGACAAC	CTTCAAATGC	TGACCCTGGG	CCCCTAACTG	ACCTGAGACT	TCAGAGCTTC	1094
TTGGGAGGAG	CTGGGGTCCC	CCAGCGGAGC	CTGGGATGGA	GCAGGGATGG	CTGCCCCAGG	1154
GAGGGGGCGG	TGGGGCCTTC	CATCCTGCTC	TGCCCTCCTC	GTCCTCTGGC	CCCAGCTCAG	1214
TCCTGTCCAT	CTCCAGCTCT	AACCATTGT	GGCCCGACAC	TGGCTCTCCC	TCTACCTTCT	1274
GTCCTTGTCT	GAACTGGTC	TCCCGTGCTC	TGGGGTCTCT	GAACTGATGG	CTGCCTCCCG	1334
CTTCTCTCCC	CTCTCCCTCT	GCCGTCTGT	CTCCTGTGGC	CAGTCTCTCC	TTGTTTCTCT	1394
TCTCCTCCTT	CCTTCTCTCC	ACCTCCCCAT	AGCCGAGCTT	GGAAAAGTCA	GACAGACCTC	1454
TGAGGTCTCA	TCCTGGAGCT	GCCACCAGCC	CAGCCTCCCT	GGGACCTGTC	TTCAGTGCCT	1514
GGGGCCCTGG	GAGCCAGGGA	GGCTCCCTGA	GGCTGAGTGA	AACTGGGCG	CTGCACCTGC	1574
CTCTCCCACG	TCCTCGGCCC	CACTCCCGCA	GGTGAGCTG	GCTGGTGACG	AAGCCCGGAG	1634
CTGGGACCAG	CAGCTCCAC	TGGGTATGGT	GGTTTCTCTC	AGGGAGCCTC	GTCATCGTCA	1694
TTGTTTGCTC	CACAGTTGGC	CTAATCATAT	GTGTGAAAAG	AAGAAAGCCA	AGGGGTGATG	1754
TAGTCAAGGT	GATCGTCTCC	GTCCAGGTAT	TGATCCTCCT	CCCCCTCTCC	CTCCCCCCTC	1814
CACCTTCCCA	CCTCCCTCT	CCCCGCTGGG	GCTGGTGTTT	CTGGTGTACA	TGGTGGGGGC	1874
TCCCAGTTCT	CTGAGGGTCC	TGAGTCTTTC	AAGTACAGCC	ACGGTAGCTC	AGGAAAGAAC	1934
CCACCCCTC	AACTGAAAG	CAGTAAAATG	AACCCGAGAA	CCTGGAGTCC	CAGGGGGGCC	1994
TGAGCAGGCA	GGGTCTCCAC	GATTCGTGTG	CTCACAGCGG	GAAAAGACAG	GAGGCAGAAG	2054
GTGAGGCCAC	AGTCATTGAG	GCCCTGCAGG	CCCCTCCGGA	CGTCACCACG	GTGGCCGTGG	2114
AGGAGACAAT	ACCCTCATTC	ACGGGGGAGG	AGCCCAAACC	ACTGACCCAC	AGACTCTGCA	2174
CCCCGACGCC	AGAGATACCT	GGAGCGACGG	CTGCTGAAAG	AGGCTGTCCA	CCTGGCGAAA	2234
CCACCGGAGC	CCGGAGGTTT	GGGGGCTCCG	CCCTGGGCTG	GTTTCCGTCT	CCTCCAGTGG	2294
AGGGAGAGGT	GGGGCCCCTG	CTGGGGTAGA	GCTGGGGACG	CCACGTGCCA	TCCCATGGG	2354
CCAGTGAGGG	CCTGGGGCCT	CTGTTCTGCT	GTGGCCTGAG	CTCCCCAGAG	TCCTGAGGAG	2414
GAGCGCCAGT	TGCCCCCTCG	TCACAGACCA	CACACCCAGC	CCTCCTGGGT	CCAGCCCAGA	2474
GGGCCCTTCA	GACCCAGCT	GTCTGCGCGT	CTGACTCTTG	TGGCCTCAGC	AGGACAGGCC	2534
CCGGGCACTG	CCTTCAAGCC	AAGGCTGGAC	TGGGTTGGCT	GCAGTGTGGT	GTTTAGTGGA	2594
TACCACATCG	GAAGTGATTT	TCTAAATTGG	ATTTGAAAAA	AAA		2637

(2) INFORMATION FOR SEQ ID NO:8:

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B3
Cont.

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Leu Gly Thr Ser Gly His Leu Val Trp Leu Ser Gln Gly Phe Ser
 1 5 10 15
 Leu Ala Gly Arg Pro Gly Ser Ser Pro Trp Pro Val Asp Ala Val Leu
 20 25 30
 Ala Cys Gly Trp Cys Pro Gly Leu His Val Pro Pro Leu Ser Pro Ser
 35 40 45
 Ser Trp Thr Pro Ala Met Gly Leu Arg Ala Ser Arg Asn Cys Ser Arg
 50 55 60
 Thr Glu Asn Ala Val Cys Gly Cys Ser Pro Gly His Phe Cys Ile Val
 65 70 75 80
 Gln Asp Gly Asp His Cys Ala Ala Cys Arg Ala Tyr Ala Thr Ser Ser
 85 90 95
 Pro Gly Gln Arg Val Gln Lys Gly Gly Thr Glu Ser Gln Asp Thr Leu
 100 105 110
 Cys Gln Asn Cys Pro Arg Gly Pro Ser Leu Pro Met Gly Pro Trp Arg
 115 120 125
 Asn Val Ser Thr Arg Pro Ser Lys
 130 135

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 1 5 10 15
 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30
 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Asp Gln
 35 40 45

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B3
Cont

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65 70 75 80

Ser-Thr Tyr Thr-Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
85 90 95

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
100 105 110

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
115 120 125

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
180 185 190

Asn Ala Ser Met Asp Ala
195

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys
1 5 10 15

Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly
20 25 30

Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
35 40 45

Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg
50 55 60

Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp
65 70 75 80

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cont.

Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu
85 90 95
Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val
100 105 110
His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala
115 120 125
Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
130 135 140
Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu
145 150

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
1 5 10 15
Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
20 25 30
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
35 40 45
Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
50 55 60
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
65 70 75 80
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
85 90 95
Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
100 105 110
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
115 120 125
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
130 135 140
Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
145 150 155 160

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Cont.

Val Cys Thr

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Cys Arg Glu Lys Gln Tyr Leu Ile Asn Ser Gln Cys Cys Ser Leu
1 5 10 15
Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Pro Thr Glu
20 25 30
Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp Thr Trp Asn
35 40 45
Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly
50 55 60
Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr Asp Thr Ile Cys Thr
65 70 75 80
Cys Glu Glu Gly Trp His Cys Thr Ser Glu Ala Cys Glu Ser Cys Val
85 90 95
Leu His Arg Ser Cys Ser Pro Gly Phe Gly Val Lys Gln Ile Ala Thr
100 105 110
Gly Val Ser Asp Thr Ile Cys Glu Pro Cys Pro Val Gly Phe Phe Ser
115 120 125
Asn Val Ser Ser Ala Phe Glu Lys Cys His Pro Trp Thr Ser Cys Glu
130 135 140
Thr Lys Asp Leu Val Val Gln Gln Ala Gly Thr Asn Lys Thr Asp Val
145 150 155 160
Val Cys Gly

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

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Cont.

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Cys Ser Asn Cys Pro Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln
 1 5 10 15
 Ile Cys Ser Pro Cys Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln
 20 25 30
 Arg Thr Cys Asp Ile Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg
 35 40 45
 Lys Glu Cys Ser Ser Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly
 50 55 60
 Phe His Cys Leu Gly Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys
 65 70 75 80
 Gln Gly Gln Glu Leu Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly
 85 90 95
 Thr Phe Asn Lys Gln Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys
 100 105 110
 Ser Leu Asp Gly Lys Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp
 115 120 125
 Val Val Cys Gly
 130

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCCCATGGC CCCAGCTCTG CCGTCCT

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCAAGCTTA TTGTGGGAGC TGCTGGTCCC

30

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGGATCCC GGAGCCCCCT GCTAC

25

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGTACCA TTGTGGGAGC TGCTGGTCCC

30

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCGCGGATCC ACCATGGAGC CTCCTGGAGA CTGG

34

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(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCGCGGTACC TCTACCCCGAG CAGGGGCGCC A

31

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGCGGATCC ACCATGGAGC CTCCTGGAGA CTGG

34

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCGCTCTAGA TCAAGCGTAG TCTGGGACGT CGTATGGGTA GTGGTTTGGG CTCCTCCC

58

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCGCGGATCC ACCATGGAGC CTCCTGGAGA CTGG

34

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGGAATTCG CAGCCATGGA GCCTCCTGGA GACTG

35

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATACCCAG GTACCCCTTC CCTCGATAGA TCTTGCCTTC GTCACCAGCC AGC

53

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cnt.